

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (withdrawn): A nucleic acid probe for measuring human gene expression, comprising:

a nucleotide sequence as set forth in any one of SEQ ID NOs: 13,701 – 27,400, the complement thereof, or a fragment of said SEQ ID NO: or said complement, wherein said probe is a single exon probe that hybridizes under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues.

Claim 2 (withdrawn): A single exon nucleic acid probe according to claim 1, wherein: said nucleotide sequence is selected from the exon SEQ ID NOs: set forth in Table 4, the complement thereof, or a fragment of said SEQ ID NO: or said complement, and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human brain.

Claim 3 (withdrawn): A single exon nucleic acid probe according to claim 1, wherein:

said nucleotide sequence is selected from the exon SEQ ID NOs: set forth in Table 5, the complement thereof, or a fragment of said SEQ ID NO: or said complement, and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human heart.

Claim 4 (withdrawn): A single exon nucleic acid probe according to claim 1, wherein: said nucleotide sequence is selected from the exon SEQ ID NOs: set forth in Table 6, the complement thereof, or a fragment of said SEQ ID NO: or said complement, and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human liver.

Claim 5 (withdrawn): A single exon nucleic acid probe according to claim 1, wherein: said nucleotide sequence is selected from the exon SEQ ID NOs: set forth in Table 7, the complement thereof, or a fragment of said SEQ ID NO: or said complement, and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human fetal liver.

Claim 6 (withdrawn): A single exon nucleic acid probe according to claim 1, wherein: said nucleotide sequence is selected from the exon SEQ ID NOs: set forth in Table 8, the complement thereof, or a fragment of said SEQ ID NO: or said complement,

and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human placenta.

Claim 7 (withdrawn): A single exon nucleic acid probe according to claim 1, wherein: said nucleotide sequence is selected from the exon SEQ ID NOs: set forth in Table 9, the complement thereof, or a fragment of said SEQ ID NO: or said complement, and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human lung.

Claim 8 (withdrawn): A single exon nucleic acid probe according to claim 1, wherein: said nucleotide sequence is selected from the exon SEQ ID NOs: set forth in Table 10, the complement thereof, or a fragment of said SEQ ID NO: or said complement, and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human bone marrow.

Claim 9 (withdrawn): A single exon nucleic acid probe according to claim 1, wherein: said nucleotide sequence is selected from the exon SEQ ID NOs: set forth in Table 11, the complement thereof, or a fragment of said SEQ ID NO: or said complement, and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in HeLa cells.

Claim 10 (withdrawn): The single exon nucleic acid probe of claim 1, wherein said fragment includes at least 20 contiguous nucleotides of said SEQ ID NO: or the complement thereof.

Claim 11 (withdrawn): The single exon nucleic acid probe of claim 1, wherein said fragment includes at least 25 contiguous nucleotides of said SEQ ID NO: or the complement thereof.

Claim 12 (withdrawn): The single exon nucleic acid probe of claim 1, wherein said fragment includes at least 50 contiguous nucleotides of said SEQ ID NO: or the complement thereof.

Claim 13 (withdrawn): The single exon nucleic acid probe of claim 1, wherein said probe further comprises, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

Claim 14 (withdrawn): The single exon nucleic acid probe of claim 13, wherein said probe further comprises, contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

Claim 15 (withdrawn): The single exon nucleic acid probe of claim 14, wherein said probe comprises a nucleotide sequence selected from any one of SEQ ID NOs: 1 - 13,700, or the complement thereof.

Claim 16 (withdrawn): The single exon nucleic acid probe of claim 15, wherein: said probe comprises a nucleotide sequence selected from the probe SEQ ID NOs: set forth in Table 4, or the complement thereof, and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human brain.

Claim 17 (withdrawn): The single exon nucleic acid probe of claim 15, wherein: said probe comprises a nucleotide sequence selected from the probe SEQ ID NOs: set forth in Table 5, or the complement thereof, and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human heart.

Claim 18 (withdrawn): The single exon nucleic acid probe of claim 15, wherein: said probe comprises a nucleotide sequence selected from the probe SEQ ID NOs: set forth in Table 6, or the complement thereof, and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human liver.

Claim 19 (withdrawn): The single exon nucleic acid probe of claim 15, wherein:
said probe comprises a nucleotide sequence selected from the probe SEQ ID NOs: set forth in Table 7, or the complement thereof,
and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human fetal liver.

Claim 20 (withdrawn): The single exon nucleic acid probe of claim 15, wherein:
said probe comprises a nucleotide sequence selected from the probe SEQ ID NOs: set forth in Table 8, or the complement thereof,
and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human placenta.

Claim 21 (withdrawn): The single exon nucleic acid probe of claim 15, wherein said probe comprises a nucleotide sequence selected from the probe SEQ ID NOs: set forth in Table 9, or the complement thereof,
and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human lung.

Claim 22 (withdrawn): The single exon nucleic acid probe of claim 15, wherein:

said probe comprises a nucleotide sequence selected from the probe SEQ ID NOs: set forth in Table 10, or the complement thereof, and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in human bone marrow.

Claim 23 (withdrawn): The single exon nucleic acid probe of claim 15, wherein: said probe comprises a nucleotide sequence selected from the probe SEQ ID NOs: set forth in Table 11, the complement thereof, or a fragment of said SEQ ID NO: or said complement, and wherein said probe hybridizes under high stringency conditions to a nucleic acid molecule expressed in HeLa cells.

Claim 24 (withdrawn): The single exon nucleic acid probe of claim 1, wherein said probe is no more than 25 kb in length.

Claim 25 (withdrawn): The single exon nucleic acid probe of claim 1, wherein said probe is no more than 5 kb in length.

Claim 26 (withdrawn): The single exon nucleic acid probe of claim 1, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

Claim 27 (withdrawn): The single exon nucleic acid probe of claim 1, wherein said probe lacks homopolymeric stretches of A or T.

Claim 28 (withdrawn): A nucleic acid probe for measuring human gene expression, comprising:

a nucleotide sequence that encodes, or the complement of which encodes, at least 8 amino acids of any one of SEQ ID NOs:27,401 - 34,288, wherein said probe is a single exon probe that hybridizes under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues.

Claim 29 (withdrawn): A spatially-addressable set of single exon nucleic acid probes for measuring human gene expression, comprising:

a plurality of single exon nucleic acid probes according to claim 1, wherein each of said plurality of probes is separately and addressably isolatable or amplifiable from said plurality.

Claim 30 (withdrawn): The spatially-addressable set of single exon nucleic acid probes of claim 29, wherein each of said plurality of probes is amplifiable using at least one common primer.

Claim 31 (withdrawn): The spatially-addressable set of single exon nucleic acid probes of claim 29, wherein said set comprises between 50 - 20,000 single exon nucleic acid probes.

Claim 32 (withdrawn): The spatially-addressable set of single exon nucleic acid probes of claim 29, wherein the average length of the single exon nucleic acid probes is between 50 bp and 750 bp.

Claim 33 (withdrawn): The spatially-addressable set of single exon nucleic acid probes of claim 29, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

Claim 34 (withdrawn): The spatially-addressable set of single exon nucleic acid probes of claim 29, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Claim 35 (withdrawn): The spatially-addressable set of single exon nucleic acid probes of claim 29, wherein said probes are addressably disposed upon a substrate.

Claim 36 (withdrawn): A single exon microarray for measuring human gene expression, comprising:

a spatially-addressable plurality of single exon nucleic acid probes according claim 1.

Claim 37 (withdrawn): A single exon microarray for measuring human gene expression, comprising:

a spatially-addressable plurality of single exon nucleic acid probes according to any one of claims 2 - 28.

Claim 38 (withdrawn): The single exon microarray of claim 36, wherein said plurality of single exon nucleic acid probes averages at least 50 bp in length.

Claim 39 (withdrawn): The single exon microarray of claim 36, wherein said plurality of single exon nucleic acid probes averages at least 75 bp in length.

Claim 40 (withdrawn): The single exon nucleic acid microarray of claim 36, wherein said single exon nucleic acid probes are noncovalently bound to the substrate of said microarray.

Claim 41 (withdrawn): A method of measuring human gene expression, comprising:
contacting the microarray of claim 36 with a first plurality of detectably labeled nucleic acids, said first plurality of nucleic acids being derived from human gene transcripts; and
then

measuring the label detectably bound to each probe of said microarray,
said measures of detected label providing a measure of human gene expression.

Claim 42 (withdrawn): The method of claim 41, further comprising:
contacting said microarray with a second plurality of detectably labeled nucleic acids;
measuring the label detectably bound to each probe of said microarray; and
comparing said first and second measurements,
said comparative measures of detected label providing a measure of human gene
expression.

Claim 43 (withdrawn): The method of claim 42, wherein said first and second pluralities
are distinguishably labeled and simultaneously contacted to said microarray.

Claim 44 (withdrawn): A vector, comprising: the single exon probe of claim 1.

Claim 45 (withdrawn): An ORF-encoded peptide, comprising: at least 8 contiguous
amino acids of any one of SEQ ID NOs:27,401 - 34,288 or at least 8 contiguous amino
acids of any one of SEQ ID NOs:27,401 - 34,288 with conservative amino acid
substitutions.

Claim 46 (withdrawn): The ORF-encoded peptide of claim 45, wherein said peptide comprises at least 15 contiguous amino acids of any one of SEQ ID NOs:27,401 - 34,288 or at least 15 contiguous amino acids of any one of SEQ ID NOs:27,401 - 34,288 with conservative amino acid substitutions.

Claim 47 (withdrawn): An isolated antibody, wherein said antibody binds specifically to a peptide according to claim 45.

Claim 48 (withdrawn): A method of selling and/or licensing single exon probes to a customer desiring to measure gene expression, comprising:
making available for computerized query a database having a plurality of records, each record corresponding to a single exon probe according to claim 1,
wherein said database responds to a customer query by returning to the customer at least one record, or an identifier of said record, that satisfies the customer query criteria, the probes to which said records correspond being available for sale and/or licensing.

Claim 49 (withdrawn): A method of selling and/or licensing single-exon microarrays to a customer desiring to measure gene expression, comprising:
making available for computerized query a database having a plurality of records, each record corresponding to a microarray according to claim 36,

wherein said database responds to a customer query by returning to the customer at least one record, or an identifier of said record, that satisfies the customer query criteria, the microarrays to which said records correspond being available for sale and/or licensing.

Claim 50 (withdrawn): A method of providing human gene expression data by subscription, comprising:
making available for computerized query a database having a plurality of records, each record including data on the expression of a single exon probe according to claim 1, wherein said database responds to a query by a customer having a subscription, but not to a query by a customer lacking such subscription, by returning at least one record, or identifier of said at least one record, that satisfies the customer query criteria.

Claim 51 (withdrawn): A computer readable storage medium storing instructions that, when executed by a computer, causes the computer to perform the method of any one of claims 48 to 51.

Claim 52 (withdrawn): A computer system, comprising a processor programmed to perform the method of any one of claims 48 to 51.

Claim 53 (withdrawn): A computer readable storage medium containing a database having a plurality of records, each record including data on the expression of a single exon probe according to claim 1.

Claim 54 (new): A method of selling and/or licensing single-exon microarrays to a customer, the method comprising:

making available for computerized query a database having a plurality of records, each record identifying a single exon microarray;

responding to a customer query of the database by returning to the customer at least one record, or an identifier of the at least one record, that identifies at least one microarray that is responsive to the customer query; and

offering for sale and/or license to the querying customer each of the at least one single exon microarrays identified in the at least one record,

wherein at least 50% of the probes addressably disposed on each of said at least one microarray are single exon probes that include a fragment of no more than one exon of a eukaryotic genome, said fragment selectively hybridizable at high stringency to an expressed gene, wherein said plurality of nucleic acid probes averages at least 100 bp in length, and wherein said eukaryotic genome averages at least one intron per gene.

Claim 55 (new): The method of claim 54, wherein at least 95% of the nucleic acid probes addressably disposed on each of said at least one microarrays includes a selectively hybridizable portion of no more than one exon of said eukaryotic genome.

Claim 56 (new): The method of claim 54, wherein at least 50% of the single exon nucleic acid probes addressably disposed on each of said at least one microarrays further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

Claim 57 (new): The method of claim 54, wherein at least 95% of said single exon nucleic acid probes addressably disposed on each of said at least one microarrays further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

Claim 58 (new): The method of claim 54, wherein at least 50% of said single exon nucleic acid probes addressably disposed on each of said at least one microarrays further comprise, (i) contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and (ii) contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

Claim 59 (new): The method of claim 54, wherein at least 95% of said single exon nucleic acid probes addressably disposed on each of said at least one microarrays further comprise, (i) contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and (ii) contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

Claim 60 (new): The method of claim 54, wherein at least 50% of said single exon nucleic acid probes addressably disposed on each of said at least one microarrays lack prokaryotic and bacteriophage vector sequence.

Claim 61 (new): The method of claim 54, wherein at least 95% of said single exon nucleic acid probes addressably disposed on each of said at least one microarrays lack prokaryotic and bacteriophage vector sequence.

Claim 62 (new): The method of claim 54, wherein at least 50% of said single exon nucleic acid probes addressably disposed on each of said at least one microarrays lack homopolymeric stretches of A or T.

Claim 63 (new): The method of claim 54, wherein at least 95% of said single exon nucleic acid probes addressably disposed on each of said at least one microarrays lack homopolymeric stretches of A or T.

Claim 64 (new): The method of claim 54, wherein said eukaryotic genome averages at least two introns per gene.

Claim 65 (new): The method of claim 54, wherein said eukaryotic genome averages at least three introns per gene.

Claim 66 (new): The method of claim 54, wherein said eukaryotic genome averages at least five introns per gene.

Claim 67 (new): The method of claim 54, wherein said genome is a human genome.

Claim 68 (new): The method of claim 54, wherein said steps of responding to customer query and offering for sale and/or license to the querying customer are performed by a digital computer.

Claim 69 (new): The method of claim 68, wherein each of said addressably disposed single exon probes comprises a nucleotide sequence selected from the group consisting of

exon SEQ ID NOs: set forth in Tables 4, 5, 6, 7, 8, 9, 10, 11, 12, and 13, and the complements thereof, and each of said single exon probes hybridizes under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues.

Claim 70 (new): The method of claim 69, wherein each of the single exon probes of at least one of said at least one microarrays comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Table 5.

Claim 71 (new): The method of claim 69, wherein said at least one microarray comprises at least a first single exon probe that includes SEQ ID NO:14193 and a second single exon probe that includes SEQ ID NO:14542.

Claim 72 (new): The method of claim 71, wherein said at least one microarray is offered for sale.

Claim 73 (new): The method of claim 71, wherein said at least one microarray is offered for license.

Claim 74 (new): A method of selling and/or licensing single exon probes to a customer, the method comprising:

making available for computerized query a database having a plurality of records, each record identifying a single exon probe;

responding to a customer query of the database by returning to the customer at least one record, or an identifier of the at least one record, that identifies at least one single exon probe that is responsive to the customer query; and

offering for sale and/or license to the querying customer each of the at least one single exon probes identified in the at least one record,

wherein each of said offered single exon probes averages at least 100 bp in length, includes a fragment of no more than one exon of a eukaryotic genome, said fragment selectively hybridizable at high stringency to an expressed gene, and wherein said eukaryotic genome averages at least one intron per gene.

Claim 75 (new): The method of claim 74, wherein at least 50% of said offered single exon probes further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

Claim 76 (new): The method of claim 75, wherein at least 50% of said offered single exon probes further comprise, (i) contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and (ii) contiguous to a second end of said fragment, a second intronic

and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

Claim 77 (new): The method of claim 74, wherein at least 50% of said offered single exon nucleic acid probes lacks prokaryotic and bacteriophage vector sequence.

Claim 78 (new): The method of claim 74, wherein at least 50% of said offered single exon nucleic acid probes lacks homopolymeric stretches of A or T.

Claim 79 (new): The method of claim 74, wherein said eukaryotic genome averages at least two introns per gene.

Claim 80 (new): The method of claim 74, wherein said eukaryotic genome averages at least three introns per gene.

Claim 81 (new): The method of claim 74, wherein said eukaryotic genome averages at least five introns per gene.

Claim 82 (new): The method of claim 74, wherein said genome is a human genome.

Claim 83 (new): The method of claim 74, wherein said steps of responding to customer query and offering for sale and/or license to the querying customer are performed by a digital computer.

Claim 84 (new): The method of claim 83, wherein each of said offered single exon probes comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Tables 4, 5, 6, 7, 8, 9, 10, 11, 12, and 13, and the complements thereof, and each of said single exon probes hybridizes under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues.

Claim 85 (new): The method of claim 84, wherein each of said offered single exon probes comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Table 5.

Claim 86 (new): The method of claim 85, wherein at least one of said offered single exon probes comprises the nucleotide sequence of exon SEQ ID NO: NO:14193.

Claim 87 (new): The method of claim 86, wherein said at least one single exon probe is offered for sale.

Claim 88 (new): The method of claim 86, wherein said at least one single exon probe is offered for license.

Claim 89 (new): A method of manufacturing a microarray that has single exon probes that share at least one customer-identified attribute in common, comprising:

receiving data from a customer that identify at least one desired common probe attribute;

identifying within a database a plurality of single exon probes having the customer-desired probe attribute; and then

addressably disposing said identified probes on a support substrate capable of functioning in microarray hybridization experiments,

wherein at least 50% of the probes addressably disposed on said microarray are single exon probes that include a fragment of no more than one exon of a eukaryotic genome, said fragment selectively hybridizable at high stringency to an expressed gene, wherein said plurality of nucleic acid probes averages at least 100 bp in length, and wherein said eukaryotic genome averages at least one intron per gene.

Claim 90 (new): The method of claim 89, wherein at least 95% of the nucleic acid probes addressably disposed on said microarray include a selectively hybridizable portion of no more than one exon of said eukaryotic genome.

Claim 91 (new): The method of claim 89, wherein at least 50% of the single exon nucleic acid probes addressably disposed on said microarray further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

Claim 92 (new): The method of claim 89, wherein at least 95% of said single exon nucleic acid probes addressably disposed on said microarray further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

Claim 93 (new): The method of claim 89, wherein at least 50% of said single exon nucleic acid probes addressably disposed said microarray further comprise, (i) contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and (ii) contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

Claim 94 (new): The method of claim 89, wherein at least 95% of said single exon nucleic acid probes addressably disposed said microarray further comprise, (i) contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and (ii) contiguous to a

second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

Claim 95 (new): The method of claim 89, wherein at least 50% of said single exon nucleic acid probes addressably disposed said microarray lack prokaryotic and bacteriophage vector sequence.

Claim 96 (new): The method of claim 89, wherein at least 95% of said single exon nucleic acid probes addressably disposed said microarray lack prokaryotic and bacteriophage vector sequence.

Claim 97 (new): The method of claim 89, wherein at least 50% of said single exon nucleic acid probes addressably disposed said microarray lack homopolymeric stretches of A or T.

Claim 98 (new): The method of claim 89, wherein at least 95% of said single exon nucleic acid probes addressably disposed said microarray lack homopolymeric stretches of A or T.

Claim 99 (new): The method of claim 89, wherein said eukaryotic genome averages at least two introns per gene.

Claim 100 (new): The method of claim 89, wherein said eukaryotic genome averages at least three introns per gene.

Claim 101 (new): The method of claim 89, wherein said eukaryotic genome averages at least five introns per gene.

Claim 102 (new): The method of claim 89, wherein said genome is a human genome.

Claim 103 (new): The method of claim 89, wherein said steps of receiving customer data and identifying within a database are performed by a digital computer.

Claim 104 (new): The method of claim 103, wherein each of said addressably disposed single exon probes comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Tables 4, 5, 6, 7, 8, 9, 10, 11, 12, and 13, and the complements thereof, and each of said single exon probes hybridizes under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues.

Claim 105 (new): The method of claim 104, wherein each of said addressably disposed single exon probes comprises a nucleotide sequence selected from the group consisting of exon SEQ ID NOs: set forth in Table 5.

Claim 106 (new): The method of claim 105, wherein said microarray comprises at least a first single exon probe that includes SEQ ID NO:14193 and second single exon probe that includes SEQ ID NO:14542.

Claim 107 (new): The method of claim 106, further comprising offering said microarray for sale and/or license.

Claim 108 (new): The method of claim 107, wherein said microarray is offered for sale.

Claim 109 (new): The method of claim 107, wherein said microarray is offered for license.